```
   1 CCGCGCCGCC GTTTGGGCCG GGWAGCGATG TAGTAGCTGC CAGGCTGTCC
  51 CCCGCCCTGC CCGGCCCGAG CCCCGCGGGC CGCCGCCGCC ACCGCCGCCA
 101 TGAAGAAGCA GTTCAACCGC ATGAAGCAGC TGGCTAACCA GACCGTGGGC
 151 AGAGCTGAGA AAACAGAAGT CCTTAGTGAA GATCTATTAC AGATTGAGAG
 201 ACGCCTGGAC ACGGTGCGGT CAATATGCCA CCATTCCCAT AAGCGCTTGG
 251 TGGCATGTTT CCAGGGCCAG CATGGCACCG ATGCCGAGAG GAGACACAAA
 301 AAACTGCCTC TGACAGCTCT TGCTCAAAAT ATGCAAGAAG CATCGACTCA
 351 GCTGGAAGAC TCTCTCCTGG GGAAGATGCT GGAGACGTGT GGAGATGCTG
 401 AGAATCAGCT GGCTCTCGAG CTCTCCCAGC ACGAAGTCTT TGTTGAGAAG
 451 GAGATCGTGG ACCCTCTGTA CGGCATAGCT GAGGTGGAGA TTCCCAACAT
 501 CCAGAAGCAG AGGAAGCAGC TTGCAAGATT GGTGTTAGAC TGGGATTCAG
 551 TCAGAGCCAG GTGGAACCAA GCTCACAAAT CCTCAGGAAC CAACTTTCAG
 601 GGGCTTCCAT CAAAAATAGA TACTCTAAAG GAAGAGATGG ATGAAGCTGG
 651 AAATAAAGTA GAACAGTGCA AGGATCAACT TGCAGCAGAC ATGTACAACT
 701 TTATGGCCAA AGAAGGGGAG TATGGCAAAT TCTTTGTTAC GTTATTAGAA
 751 GCCCAAGCAG ATTACCATAG AAAAGCATTA GCAGTCTTAG AAAAGACCCT
 801 CCCCGAAATG CGAGCCCATC AAGATAAGTG GGCGGAAAAA CCAGCCTTTG
 851 GGACTCCCCT AGCAGAACAC CTGAAGAGGA GCGGGCGCGA GATTGCGCTG
 901 CCCATTGAAG CCTGTGTCAT GCTGCTTCTG GAGACAGGCA TGAAGGAGGA
 951 GGGCCTTTTC CGAATTGGGG CTGGGGCCTC CAAGTTAAAG AAGCTGAAAG
1001 CTGCTTTGGA CTGTTCTACT TCTCACCTGG ATGAGTTCTA TTCAGACCCC
1051 CATGCTGTAG CAGGTGCTTT AAAATCCTAT TTACGGGAAT TGCCTGAACC
1101 TTTGATGACT TTTAATCTGT ATGAAGAATG GACACAAGTT GCAAGTGTGC
1151 AGGATCAAGA CAAAAAACTT CAAGACTTGT GGAGAACATG TCAGAAGTTG
1201 CCACCACAAA ATTTTGTTAA CTTTAGATAT TTGATCAAGT TCCTTGCAAA
1251 GCTTGCTCAG ACCAGCGATG TGAATAAAAT GACTCCCAGC AACATTGCGA
1301 TTGTGTTAGG CCCTAACTTG TTATGGGCCA GAAATGAAGG GACACTTGCT
1351 GAAATGGCAG CAGCCACATC CGTCCATGTG GTTGCAGTGA TTGAACCCAT
1401 CATTCAGCAT GCCGACTGGT TCTTCCCTGA AGAGGTGGAA TTTAATGTAT
1451 CAGAAGCATT TGTACCTCTC ACCACCCCGA GTTCTAATCA CTCATTCCAC
1501 ACTGGAAACG ACTCTGACTC GGGGACCCTG GAGAGGAAGC GGCCTGCTAG
1551 CATGGCGGTG ATGGAAGGAG ACTTGGTGAA GAAGGAAAGT CCTCCCAAAC
1601 CGAAGGACCC TGTATCTGCA GCTGTGCCAG CACCAGGGAG AAACAACAGT
1651 CAGATAGCAT CTGGCCAAAA TCAGCCCCAG GCAGCTGCTG GCTCCCACCA
1701 GCTCTCCATG GGCCAACCTC ACAATGCTGC AGGGCCCAGC CCGCATACAC
1751 TGCGCCGAGC TGTTAAAAAA CCCGCTCCAG CACCCCCGAA ACCGGGCAAC
1801 CCACCTCCTG GCCACCCCGG GGGCCAGAGT TCTTCAGGAA CATCTCAGCA
1851 TCCACCCAGT CTGTCACCAA AGCCACCCAC CCGAAGCCCC TCTCCTCCCA
1901 CCCAGCACAC GGGCCAGCCT CCAGGCCAGC CCTCCGCCCC CTCCCAGCTC
1951 TCAGCACCCC GGAGGTACTC CAGCAGCTTG TCTCCAATCC AAGCTCCCAA
2001 TCACCCACCG CCGCAGCCCC CTACGCAGGC CACGCCACTG ATGCACACCA
2051 AACCCAATAG CCAGGGCCCT CCCAACCCCA TGGCATTGCC CAGTGAGCAT
2101 GGACTTGAGC AGCCATCTCA CACCCCTCCC CAGACTCCAA CGCCCCCCAG
2151 TACTCCGCCC CTAGGAAAAC AGAACCCCAG TCTGCCAGCT CCTCAGACCC
2201 TGGCAGGGGG TAACCCTGAA ACTGCACAGC CACATGCTGG AACCTTACCG
2251 AGACCGAGAC CAGTACCAAA GCCAAGGAAC CGGCCCAGCG TGCCCCCACC
2301 CCCCCAACCT CCTGGTGTCC ACTCAGCTGG GGACAGCAGC CTCACCAACA
2351 CAGCACCAAC AGCTTCCAAG ATAGTAACAG ACTCCAATTC CAGGGTTTCA
2401 GAACCGCATC GCAGCATCTT TCCTGAAATG CACTCAGACT CAGCCAGCAA
2451 AGACGTGCCT GGCCGCATCC TGCTGGATAT AGACAATGAT ACCGAGAGCA
2501 CTGCCCTGTG AAGAAAGCCC TTTCCCAGCC CTCCACCACT TCCACCCTGG
2551 CGAGTGGAGC AGGGGCAGGC GAACCTCTTT CTTTGCAGAC CGAACAGTGA
2601 AAAGCTTTCA GTGGAGGACA AAGGAGGGCC TCACTGTGCG GGACCTGGCC
2651 TTCTGCACGG CCCAAGGAGA ACCTGGAGGC CACCACTAAA GCTGAATGAC
2701 CTGTGTCTTG AAGAAGTTGG CTTTCTTTAC ATGGGAAGGA AATCATGCCA
2751 AAAAAATCCA AAACAAAGAA GTACCTGGAG TGGAGAGAGT ATTCCTGCTG
2801 AAACGCGCAT AGGAAGCTTT TGTCCCTGCT GTTAATGCGG GCAGCACCTA
2851 CAGCAACTTG GAATGAGTAA GAAGCAGTGC GTTAACTATC TATTTAATAA
2901 AATGCGCTCA TTATGCAAGT CGCCTACTCT CTGCTACCTG GACGTTCATT
2951 CTTATGTATT AGGAGGGAGG CTGCGCTCCT TCAGACTTGC TGCAGAATCA
3001 TTTTGTATCA TGTATGGTCT GTGTCTCCCC AGTCCCCTCA GAACCATGCC
3051 CATGGATGGT GACTGCTGGC TCTGTCACCT CATCAAACTG GATGTGACCC
3101 ATGCCGCCTC GTTGGATTGT CGGAATGTAG ACAGAAATGT ACTGTTCTTT
```

FIGURE 1, page 1 of 2

3151 TTTTTTTTTT TAAACAATGT AATTGCTACT TGATAAGGAC CGAACATTAT
3201 TCTAGTTTCA TGTTTAATTT GAATTAAATA TATTCTGTGG TTTATATG

FEATURES:
5'UTR: 1-99
Start Codon: 100
Stop Codon: 2509
3'UTR: 2512

Homologous proteins:
Top 10 BLAST Hits

	Score	E
CRA|147000022595308 /altid=gi|10435148 /def=dbj|BAB14506.1| (AK...	1500	0.0
CRA|335001098671246 /altid=gi|11560044 /def=ref|NP_071580.1| na...	1331	0.0
CRA|18000005158484 /altid=gi|7662242 /def=ref|NP_055674.1| KIAA...	645	0.0
CRA|335001098684832 /altid=gi|11425473 /def=ref|XP_008288.1| KI...	645	0.0
CRA|335001098688185 /altid=gi|11431577 /def=ref|XP_007992.1| hy...	452	e-126
CRA|335001098646266 /altid=gi|11545733 /def=ref|NP_061830.1| SH...	421	e-116
CRA|18000004990129 /altid=gi|6677931 /def=ref|NP_033190.1| SH3-...	390	e-107
CRA|89000000202138 /altid=gi|7300563 /def=gb|AAF55715.1| (AE003...	264	3e-69
CRA|66000019404309 /altid=gi|8922344 /def=ref|NP_060524.1| homo...	251	2e-65
CRA|18000005246399 /altid=gi|7512523 /def=pir||T12533 hypotheti...	190	4e-47

EST:

gi|10993873 /dataset=dbest /taxon=96...	1524	0.0
gi|11003732 /dataset=dbest /taxon=96...	1495	0.0
gi|12040806 /dataset=dbest /taxon=96...	1170	0.0
gi|10948137 /dataset=dbest /taxon=96...	1049	0.0
gi|11303345 /dataset=dbest /taxon=96...	1043	0.0
gi|7933255 /dataset=dbest /taxon=960...	918	0.0
gi|10332226 /dataset=dbest /taxon=96...	912	0.0
gi|11643637 /dataset=dbest /taxon=96...	906	0.0
gi|10348166 /dataset=dbest /taxon=960...	664	0.0
gi|4753575 /dataset=dbest /taxon=9606 ...	609	e-171

EXPRESSION INFORMATION FOR MODULATORY USE:
library source:
Expression information from BLAST dbEST hits:

gi|10993873	Neuronal teratocarcinoma
gi|11003732	Umbilical vein endothelial cell
gi|12040806	Iris
gi|10948137	Teratocarcinoma
gi|11303345	Breast
gi|7933255	Leiomios
gi|10332226	Uterus
gi|11643637	Kidney renal carcinoma (ascites)
gi|10348166	Uterus leiomyosarcoma
gi|4753575	Human fetal heart

Expression information from PCR-based tissue screening panels:
Human leukocytes

FIGURE 1, page 2 of 2

```
   1 MKKQFNRMKQ LANQTVGRAE KTEVLSEDLL QIERRLDTVR SICHHSHKRL
  51 VACFQGQHGT DAERRHKKLP LTALAQNMQE ASTQLEDSLL GKMLETCGDA
 101 ENQLALELSQ HEVFVEKEIV DPLYGIAEVE IPNIQKQRKQ LARLVLDWDS
 151 VRARWNQAHK SSGTNFQGLP SKIDTLKEEM DEAGNKVEQC KDQLAADMYN
 201 FMAKEGEYGK FFVTLLEAQA DYHRKALAVL EKTLPEMRAH QDKWAEKPAF
 251 GTPLAEHLKR SGREIALPIE ACVMLLLETG MKEEGLFRIG AGASKLKKLK
 301 AALDCSTSHL DEFYSDPHAV AGALKSYLRE LPEPLMTFNL YEEWTQVASV
 351 QDQDKKLQDL WRTCQKLPPQ NFVNFRYLIK FLAKLAQTSD VNKMTPSNIA
 401 IVLGPNLLWA RNEGTLAEMA AATSVHVVAV IEPIIQHADW FFPEEVEFNV
 451 SEAFVPLTTP SSNHSFHTGN DSDSGTLERK RPASMAVMEG DLVKKESPPK
 501 PKDPVSAAVP APGRNNSQIA SGQNQPQAAA GSHQLSMGQP HNAAGPSPHT
 551 LRRAVKKPAP APPKPGNPPP GHPGGQSSSG TSQHPPSLSP KPPTRSPSPP
 601 TQHTGQPPGQ PSAPSQLSAP RRYSSSLSPI QAPNHPPPQP PTQATPLMHT
 651 KPNSQGPPNP MALPSEHGLE QPSHTPPQTP TPPSTPPLGK QNPSLPAPQT
 701 LAGGNPETAQ PHAGTLPRPR PVPKPRNRPS VPPPPQPPGV HSAGDSSLTN
 751 TAPTASKIVT DSNSRVSEPH RSIFPEMHSD SASKDVPGRI LLDIDNDTES
 801 TAL
```

FEATURES:
Functional domains and key regions:
[1] PDOC00001 PS00001 ASN_GLYCOSYLATION
N-glycosylation site

Number of matches: 6

1	13-16	NQTV
2	449-452	NVSE
3	463-466	NHSF
4	470-473	NDSD
5	515-518	NNSQ
6	796-799	NDTE

[2] PDOC00004 PS00004 CAMP_PHOSPHO_SITE
cAMP- and cGMP-dependent protein kinase phosphorylation site

Number of matches: 2

1	494-497	KKES
2	621-624	RRYS

[3] PDOC00005 PS00005 PKC_PHOSPHO_SITE
Protein kinase C phosphorylation site

Number of matches: 7

1	38-40	TVR
2	46-48	SHK
3	150-152	SVR
4	175-177	TLK
5	261-263	SGR
6	550-552	TLR
7	589-591	SPK

[4] PDOC00006 PS00006 CK2_PHOSPHO_SITE
Casein kinase II phosphorylation site

Number of matches: 14

1	60-63	TDAE
2	83-86	TQLE
3	96-99	TCGD
4	109-112	SQHE
5	171-174	SKID
6	175-178	TLKE
7	214-217	TLLE
8	233-236	TLPE
9	261-264	SGRE
10	308-311	SHLD
11	349-352	SVQD
12	415-418	TLAE
13	468-471	TGND
14	742-745	SAGD

[5] PDOC00007 PS00007 TYR_PHOSPHO_SITE
Tyrosine kinase phosphorylation site

117-124 KEIVDPLY

[6] PDOC00008 PS00008 MYRISTYL
N-myristoylation site

Number of matches: 10

1	56-61	GQHGTD
2	251-256	GTPLAE
3	290-295	GAGASK
4	322-327	GALKSY
5	538-543	GQPHNA
6	574-579	GGQSSS
7	575-580	GQSSSG
8	605-610	GQPPGQ
9	704-709	GNPETA
10	739-744	GVHSAG

[7] PDOC00161 PS00178 AA_TRNA_LIGASE_I
Aminoacyl-transfer RNA synthetases class-I signature

706-716 PETAQPHAGTL

Membrane spanning structure and domains:

Helix	Begin	End	Score	Certainty
1	415	435	0.842	Putative

BLAST Alignment to Top Hit:

>CRA|147000022595308 /altid=gi|10435148 /def=dbj|BAB14506.1|
(AK023281) unnamed protein product [Homo sapiens]
/org=Homo sapiens /taxon=9606 /dataset=nraa /length=726
Length = 726

Score = 1500 bits (3840), Expect = 0.0
Identities = 726/726 (100%), Positives = 726/726 (100%)

```
Query: 78  MQEASTQLEDSLLGKMLETCGDAENQLALELSQHEVFVEKEIVDPLYGIAEVEIPNIQKQ 137
           MQEASTQLEDSLLGKMLETCGDAENQLALELSQHEVFVEKEIVDPLYGIAEVEIPNIQKQ
Sbjct: 1   MQEASTQLEDSLLGKMLETCGDAENQLALELSQHEVFVEKEIVDPLYGIAEVEIPNIQKQ 60

Query: 138 RKQLARLVLDWDSVRARWNQAHKSSGTNFQGLPSKIDTLKEEMDEAGNKVEQCKDQLAAD 197
           RKQLARLVLDWDSVRARWNQAHKSSGTNFQGLPSKIDTLKEEMDEAGNKVEQCKDQLAAD
Sbjct: 61  RKQLARLVLDWDSVRARWNQAHKSSGTNFQGLPSKIDTLKEEMDEAGNKVEQCKDQLAAD 120

Query: 198 MYNFMAKEGEYGKFFVTLLEAQADYHRKALAVLEKTLPEMRAHQDKWAEKPAFGTPLAEH 257
           MYNFMAKEGEYGKFFVTLLEAQADYHRKALAVLEKTLPEMRAHQDKWAEKPAFGTPLAEH
Sbjct: 121 MYNFMAKEGEYGKFFVTLLEAQADYHRKALAVLEKTLPEMRAHQDKWAEKPAFGTPLAEH 180

Query: 258 LKRSGREIALPIEACVMLLLETGMKEEGLFRIGAGASKLKKLKAALDCSTSHLDEFYSDP 317
           LKRSGREIALPIEACVMLLLETGMKEEGLFRIGAGASKLKKLKAALDCSTSHLDEFYSDP
Sbjct: 181 LKRSGREIALPIEACVMLLLETGMKEEGLFRIGAGASKLKKLKAALDCSTSHLDEFYSDP 240

Query: 318 HAVAGALKSYLRELPEPLMTFNLYEEWTQVASVQDQDKKLQDLWRTCQKLPPQNFVNFRY 377
           HAVAGALKSYLRELPEPLMTFNLYEEWTQVASVQDQDKKLQDLWRTCQKLPPQNFVNFRY
Sbjct: 241 HAVAGALKSYLRELPEPLMTFNLYEEWTQVASVQDQDKKLQDLWRTCQKLPPQNFVNFRY 300

Query: 378 LIKFLAKLAQTSDVNKMTPSNIAIVLGPNLLWARNEGTLAEMAAATSVHVVAVIEPIIQH 437
           LIKFLAKLAQTSDVNKMTPSNIAIVLGPNLLWARNEGTLAEMAAATSVHVVAVIEPIIQH
Sbjct: 301 LIKFLAKLAQTSDVNKMTPSNIAIVLGPNLLWARNEGTLAEMAAATSVHVVAVIEPIIQH 360

Query: 438 ADWFFPEEVEFNVSEAFVPLTTPSSNHSFHTGNDSDSGTLERKRPASMAVMEGDLVKKES 497
           ADWFFPEEVEFNVSEAFVPLTTPSSNHSFHTGNDSDSGTLERKRPASMAVMEGDLVKKES
Sbjct: 361 ADWFFPEEVEFNVSEAFVPLTTPSSNHSFHTGNDSDSGTLERKRPASMAVMEGDLVKKES 420

Query: 498 PPKPKDPVSAAVPAPGRNNSQIASGQNQPQAAAGSHQLSMGQPHNAAGPSPHTLRRAVKK 557
           PPKPKDPVSAAVPAPGRNNSQIASGQNQPQAAAGSHQLSMGQPHNAAGPSPHTLRRAVKK
Sbjct: 421 PPKPKDPVSAAVPAPGRNNSQIASGQNQPQAAAGSHQLSMGQPHNAAGPSPHTLRRAVKK 480

Query: 558 PAPAPPKPGNPPPGHPGGQSSSGTSQHPPSLSPKPPTRSPSPPTQHTGQPPGQPSAPSQL 617
           PAPAPPKPGNPPPGHPGGQSSSGTSQHPPSLSPKPPTRSPSPPTQHTGQPPGQPSAPSQL
Sbjct: 481 PAPAPPKPGNPPPGHPGGQSSSGTSQHPPSLSPKPPTRSPSPPTQHTGQPPGQPSAPSQL 540

Query: 618 SAPRRYSSSLSPIQAPNHPPPQPPTQATPLMHTKPNSQGPPNPMALPSEHGLEQPSHTPP 677
           SAPRRYSSSLSPIQAPNHPPPQPPTQATPLMHTKPNSQGPPNPMALPSEHGLEQPSHTPP
Sbjct: 541 SAPRRYSSSLSPIQAPNHPPPQPPTQATPLMHTKPNSQGPPNPMALPSEHGLEQPSHTPP 600

Query: 678 QTPTPPSTPPLGKQNPSLPAPQTLAGGNPETAQPHAGTLPRPRPVPKPRNRPSVPPPPQP 737
           QTPTPPSTPPLGKQNPSLPAPQTLAGGNPETAQPHAGTLPRPRPVPKPRNRPSVPPPPQP
Sbjct: 601 QTPTPPSTPPLGKQNPSLPAPQTLAGGNPETAQPHAGTLPRPRPVPKPRNRPSVPPPPQP 660

Query: 738 PGVHSAGDSSLTNTAPTASKIVTDSNSRVSEPHRSIFPEMHSDSASKDVPGRILLDIDND 797
           PGVHSAGDSSLTNTAPTASKIVTDSNSRVSEPHRSIFPEMHSDSASKDVPGRILLDIDND
Sbjct: 661 PGVHSAGDSSLTNTAPTASKIVTDSNSRVSEPHRSIFPEMHSDSASKDVPGRILLDIDND 720

Query: 798 TESTAL 803
           TESTAL
Sbjct: 721 TESTAL 726
```

>CRA|335001098671246 /altid=gi|11560044 /def=ref|NP_071580.1|

```
nadrin; neuron-specific GTPase activating protein
[Rattus norvegicus] /org=Rattus norvegicus /taxon=10116
/dataset=nraa /length=780
Length = 780

Score = 1331 bits (3406), Expect = 0.0
Identities = 676/816 (82%), Positives = 697/816 (84%), Gaps = 49/816 (6%)

Query: 1   MKKQFNRMKQLANQTVGRAEKTEVLSEDLLQIERRLDTVRSICHHSHKRLVACFQGQHGT 60
            MKKQFNRMKQLANQTVGRAEKTEVLSEDLLQIERRLDTVRS+CHHSHKRL+ACFQGQHGT
Sbjct: 1   MKKQFNRMKQLANQTVGRAEKTEVLSEDLLQIERRLDTVRSMCHHSHKRLIACFQGQHGT 60

Query: 61  DAERRHKKLPLTALAQNMQEASTQLEDSLLGKMLETCGDAENQLALELSQHEVFVEKEIV 120
            DAERRHKKLPLTALAQNMQEAS QLE+SLLGKMLETCGDAENQLA ELSQHEVFVEKEI+
Sbjct: 61  DAERRHKKLPLTALAQNMQEASAQLEESLLGKMLETCGDAENQLAFELSQHEVFVEKEIM 120

Query: 121 DPLYGIAEVEIPNIQKQRKQLARLVLDWDSVRARWNQAHKSSGTNFQGLPSKIDTLKEEM 180
            DPLYGIAEVEIPNIQKQRKQLARLVLDWDSVRARWNQAHKSSGTNFQGLPSKIDTLKEEM
Sbjct: 121 DPLYGIAEVEIPNIQKQRKQLARLVLDWDSVRARWNQAHKSSGTNFQGLPSKIDTLKEEM 180

Query: 181 DEAGNKVEQCKDQLAADMYNFMAKEGEYGKFFVTLLEAQADYHRKALAVLEKTLPEMRAH 240
            DEAGNKVEQCKDQLAADMYNFMAKEGEYGKFFVTLLEAQADYHRKALAVLEK LPEMRAH
Sbjct: 181 DEAGNKVEQCKDQLAADMYNFMAKEGEYGKFFVTLLEAQADYHRKALAVLEKALPEMRAH 240

Query: 241 QDKWAEKPAFGTPLAEHLKRSGREIALPIEACVMLLLETGMKEEGLFRIGAGASKLKKLK 300
            QDKWAEKPAFGTPL EHLKRSGREIALPIEACVMLLLETGMKEEGLFRIGAGASKLKKLK
Sbjct: 241 QDKWAEKPAFGTPLEEHLKRSGREIALPIEACVMLLLETGMKEEGLFRIGAGASKLKKLK 300

Query: 301 AALDCSTSHLDEFYSDPHAVAGALKSYLRELPEPLMTFNLYEEWTQVASVQDQDKKLQDL 360
            AALDCSTSHLDEFYSDPHAVAGALKSYLRELPEPLMTF+LYEEWTQVASVQDQDKKLQ L
Sbjct: 301 AALDCSTSHLDEFYSDPHAVAGALKSYLRELPEPLMTFSLYEEWTQVASVQDQDKKLQYL 360

Query: 361 WRTCQKLPPQNFVNFRYLIKFLAKLAQTSDVNKMTPSNIAIVLGPNLLWARNEGTLAEMA 420
            W TCQKLPPQNFVNFRYLIKFLAKLAQTSDVNKMTPSNIAIVLGPNLLWA+ EGTLAE+A
Sbjct: 361 WTTCQKLPPQNFVNFRYLIKFLAKLAQTSDVNKMTPSNIAIVLGPNLLWAKQEGTLAEIA 420

Query: 421 AATSVHVVAVIEPIIQHADWFFPEEVEFNVSEAFVPLTTPSSNHSFHTGNDSDSGTLERK 480
            AATSVHVVAVIEPIIQHADWFFP EVEFNVSEAFVPL TP+SNHS HTGNDSDSGTLERK
Sbjct: 421 AATSVHVVAVIEPIIQHADWFFPGEVEFNVSEAFVPLATPNSNHSSHTGNDSDSGTLERK 480

Query: 481 RPASMAVMEGDLVKKESPPKPKDPVSAAVPAPGRNNSQIASGQNQPQAAAGSHQLSMGQP 540
            RPASMAVMEGDLVKKESPPKPKD VSAA P  GRN++QI +  NQ Q    SHQLS+G
Sbjct: 481 RPASMAVMEGDLVKKESPPKPKDSVSAAAPVAGRNSNQITTVPNQAQTGGNSHQLSVGTA 540

Query: 541 HNAAGPSPHTLRRAVKKPAPAPPKPGNPPPGHPGGQSSSGTSQHPPSLSPKPPTRSPSPP 600
            H+AAGPSPHTLRRAVKKPAPAPPKPGNPPPGHPGGQSS GT       SPKP TRSPSPP
Sbjct: 541 HSAAGPSPHTLRRAVKKPAPAPPKPGNPPPGHPGGQSSPGT-----GTSPKPSTRSPSPP 595

Query: 601 -------------TQHTGQPPGQPSAPSQLSAPRRYSSSLSPIQAPNHPPPQPPTQATPL 647
                          Q   Q   Q     Q    RR SSSL PIQAPNHPPPQPPTQ
Sbjct: 596 QQQQQQQQQQQQQQQQQQQQQQQQQQQQQTPGMRRCSSSLPPIQAPNHPPPQPPTQ---- 651

Query: 648 MHTKPNSQGPPNPMALPSEHGLEQPSHTPPQTPTPPSTPPLGKQNPSLPAPQTLAGGNPE 707
               +   QGP             +P  TPPQTPTPPSTPP  KQN S            E
Sbjct: 652 --PRLGEQGP-------------EPGPTPPQTPTPPSTPPPAKQNSS----------QSE 686

Query: 708 TAQPHAGTLPRPRPVPKPRNRPSVPPPPQPPGVHSAGDSSLTNTAPTASKIVTDSNSRVS 767
            T Q H GTLPRPRPVPKPRNRPSVPPPP PPG H  GD  LT + PTAS+IVTD+NSRVS
Sbjct: 687 TTQLH-GTLPRPRPVPKPRNRPSVPPPPNPPGTH-MGDGGLTPSVPTASRIVTDTNSRVS 744

Query: 768 EPHRSIFPEMHSDSASKDVPGRILLDIDNDTESTAL 803
            E  R+IFPE+HSD ASK+VPG ILLDIDNDTESTAL
Sbjct: 745 ESLRNIFPEIHSDLASKEVPGHILLDIDNDTESTAL 780
```

FIGURE 2, page 4 of 5

Hmmer search results (Pfam):

Model	Description	Score	E-value	N
PF00620	RhoGAP domain	191.2	1.6e-53	1

Parsed for domains:

Model	Domain	seq-f	seq-t		hmm-f	hmm-t		score	E-value
PF00620	1/1	266	415	..	1	170	[]	191.2	1.6e-53

FIGURE 2, page 5 of 5

```
   1 CTCGTGGCTG AGTTTAATTA CACACTCTTG CTCTAGCTGT AAGGCAGAGC
  51 TCTCCAGGTT AGCTTCAGTG GACAATCTTT TCATGGTTTT CTCAGAGTTG
 101 TTTCTTCCAA TAGCCTCTTT TCAGCTAGGG GTCTCACTCT GTCACCCAGA
 151 CAAGAGTGCA ATGGTGTGAT AATAGCTCAC TGCAGCCTCA AATTCCTGGG
 201 CTCAAATGAT CCTGTTGCCT CAGCCTTTCA ACTAGTTGGG AGTACAGGTG
 251 CATGCCACTG CTTCTGGCCT TTTTTTTTTT TTTAAATTTT TCATAGAGAT
 301 GAGGTTTTAG TATGTTGTCC AGGCTAGTCT CATACTCCTG AGCTCAAGTG
 351 ATCTTCCCAT CTTGACCTCC CAAAGTGCTA GGATTACAGG TGTGAGCCAC
 401 TGCACCTGGC CCCAGAAGAT AATTTTTTAT TTGTCTTTTA CTCTATGTTC
 451 AAATTCTTCA ATTTTTTGGT AGACTCTACT TTTTCAATTT GTAGAGCTTG
 501 CATGAATAGT GTTTTCCTTC TCTTGAAGTT TAGAGAGATC ATGTACTGTA
 551 ATTCCTGAGC CACCTTGCTG TAACAAATTT TCCAGTTCTT CAATCTTTTC
 601 TTCCTAATTG CTTAGATTTT CTTGATGCTT ACAACTTATT TCCCTCAATT
 651 TCTGTTGATG AACATTCTGT AATACTGATA ATTCAAGCTG ATGGTCATCA
 701 GTATCCTGAC TTCTTTTTTG TTTGAGCTCC TTGATGATAT TAATATTTGG
 751 TGTTTGTAGT TTGTAGATTT CATTTTCATC AAAACTAGTT GTTCCTCCTA
 801 TTTTATAAGT CTGAGCAATA CATTTCCAAT GGCCAACTGG AGACTCAAGT
 851 TTTAGAACTT CATTGGACTA TCTGTTTATT TCTTGTTATG ATGAAATTAT
 901 GTCATAAAAA CCCATGTAAG CGTCGTGGAA CACTGAAGCA TGATGGGTAC
 951 CACATGGAAT GGAGGGGATG CAGTGTGGAT GGGAACCTCC GGCCTTCCCT
1001 GAATGTGCTG ACTCCAGGGC TGGCTGCCGG TCCTGCAACC GATCCTGTAG
1051 TGCTTGCTTT CTTGTTTTAG GAAGGCTCAT TTCTACCTCT TTCTGTTGTA
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15451 AGACAGGGTT TCGCTTTGGT CAGATTGGTC TTGAACTCCT GACCTCAGGT
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15551 CTGCACCTAG CCTGCATCAG TATGGTTTAA TAACTGTTGA TCTGTAATAT
15601 GTTTTAAATT GGGTAGAGCT GGTCTCTTAC AAATACTCTT TTTCAGGCTG
15651 GGTTTGTGGC TCACGCCTGT AATCCCCAGC ACTTTGGAAA GCTGAGGCCG
15701 GAGGATCGCT TGAGGCCAGG AGTTCAAGGC TGCAGTGAGC TGTGGTCCTG

FIGURE 3, page 5 of 33

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17401 TGTGTGCTAG GGAGGCGTCA TGAGACAGTG AGGACATACA GTGTGACACA
17451 GCAGGTCAGC ACTGGGGAAA ATAGCCAGGT TAGCCTTCAC TTCACTGCTC
17501 TATGCCAAAA TACATTCCAA ATGGGTTAAA GCTTTCATGT AAAAAATAAA
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CHROMOSOME MAP POSITION:
Chromosome 16